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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Mahajan et al.	Date:	September 5, 2001
Serial No.:	09/537,654	Group Art Unit:	1638
Filed:	March 29, 2000	Examiner:	Kubelik, A.
For:	"A Novel Maize Rad51-Like Gene and Uses Thereof		

Assistant Commissioner for Patents
Washington, D.C. 20231

Response to Restriction Requirement

This is in response to the Restriction Requirement issued August 8, 2001, in which the Examiner has required restriction between Group I (Claims 1-10) and Group II (Claim 11) as well as a non-species sequence election. Applicants hereby elect with traverse to prosecute the claims of Group I, SEQ ID NO: 1 and expressly reserve the right to file divisional applications or take other such appropriate measures to protect the inventions in the remaining claims. No change of inventorship is required due to this election of Group I, SEQ ID NO: 1. The Applicants respectfully traverse the Restriction Requirement and request reconsideration of the same.

The Examiner has concluded that inventions I and II are unrelated. Inventions are unrelated if it can be shown that they are not disclosed as capable of

use together and they have different modes of operation, different functions, or different effects. The Examiner asserts that the different inventions have different modes of operation and different functions. The Applicants respectfully traverse. Inventions of Groups I and II are capable of use together as a polynucleotide of Group I can be used to produce the polypeptide of Group II using the method of Group I. As such, Claim 9 is directed to this process and may be considered a unifying claim. The inventions of Groups I and II have the same function as in Claim 9, that is, to modulate the level of Rad51. Further, Claim 1 (b) is directed to any polynucleotide that encodes a polypeptide of SEQ ID NOS: 2, 4, or 6, again linking these two Groups. Also, it is believed that Group I and Group II can be searched together without an undue burden on the Examiner.

Further, the Examiner has required a non-species sequence election. Applicants respectfully traverse. Sequences of SEQ ID NOS: 1, 3, and 5 of the elected group are all highly related Rad51 polynucleotides. An alignment of SEQ ID NOS: 1, 3, and 5 is included to show their high homology, as well as pairwise GAP analyses of each possible pair. These analyses show that SEQ ID NOS: 1 and 5 are the least identical with a GAP percent identity score of 98.65%. The majority of the difference is due to differences in the UTR's of the sequences as is illustrated by the GAP analysis of the encoded polypeptides discussed below. Further, an alignment of SEQ ID NOS: 2, 4, and 6 is provided, as well as pairwise GAP analyses of all possible pairs. These analyses show that SEQ ID NOS: 2 and 6 are 100% identical, SEQ ID NOS: 1 and 5 encode identical polypeptides. Further, GAP analyses show that SEQ ID NOS: 2 or 6 vs. 4 have 99.644% sequence identity, essentially identical polypeptides. Due to this extremely high percent identity, it is believed that SEQ ID NOS: 1, 3, and 5 can be searched together without an undue burden on the Examiner.

Further, it would be an unreasonable burden on the Applicant to file divisional applications to protect all the sequences of the invention if only one sequence will be

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examined in each application. The MPEP § 803.04 allows some discretion in the examination and restriction practice in regards to sequences, allowing "up to ten independent and distinct nucleotide sequences" to be examined in a single application. As such, the Applicants request that the Examiner use this discretion to rejoin the sequences into this application. Therefore, the Applicants respectfully request that restriction between Groups I, and II, as well as the sequence election of one of SEQ ID NOS: 1 - 6 in this application be withdrawn.

Respectfully submitted,



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